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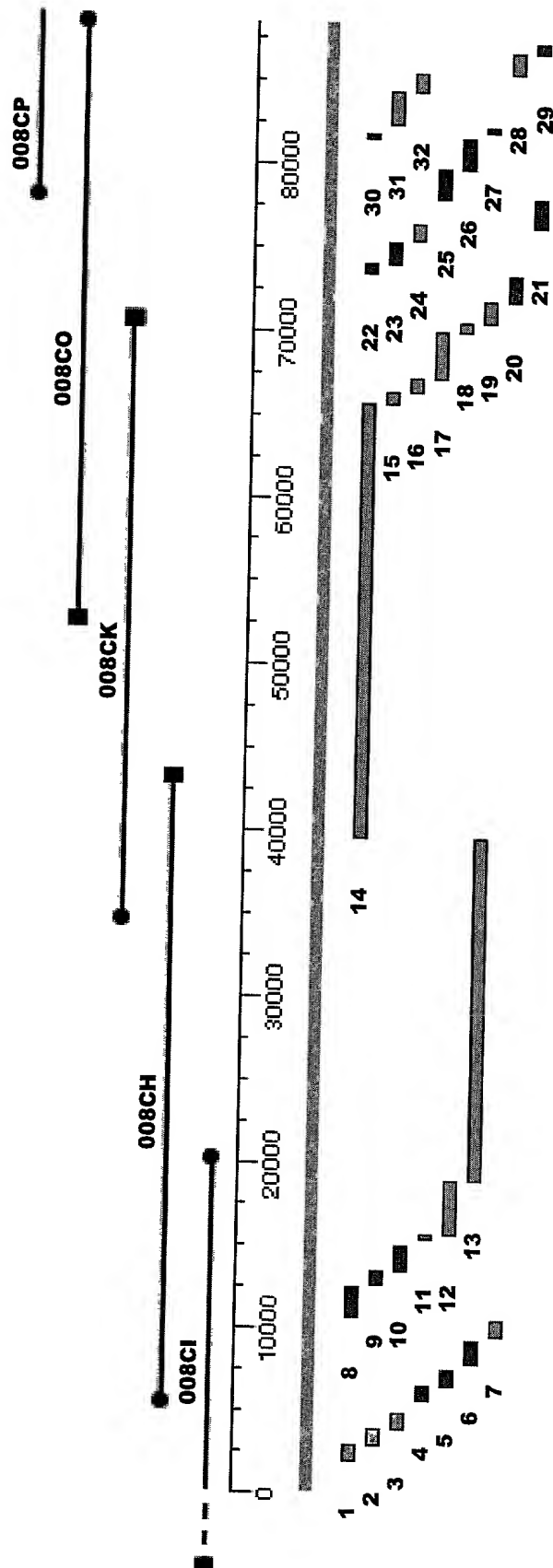


Figure 1

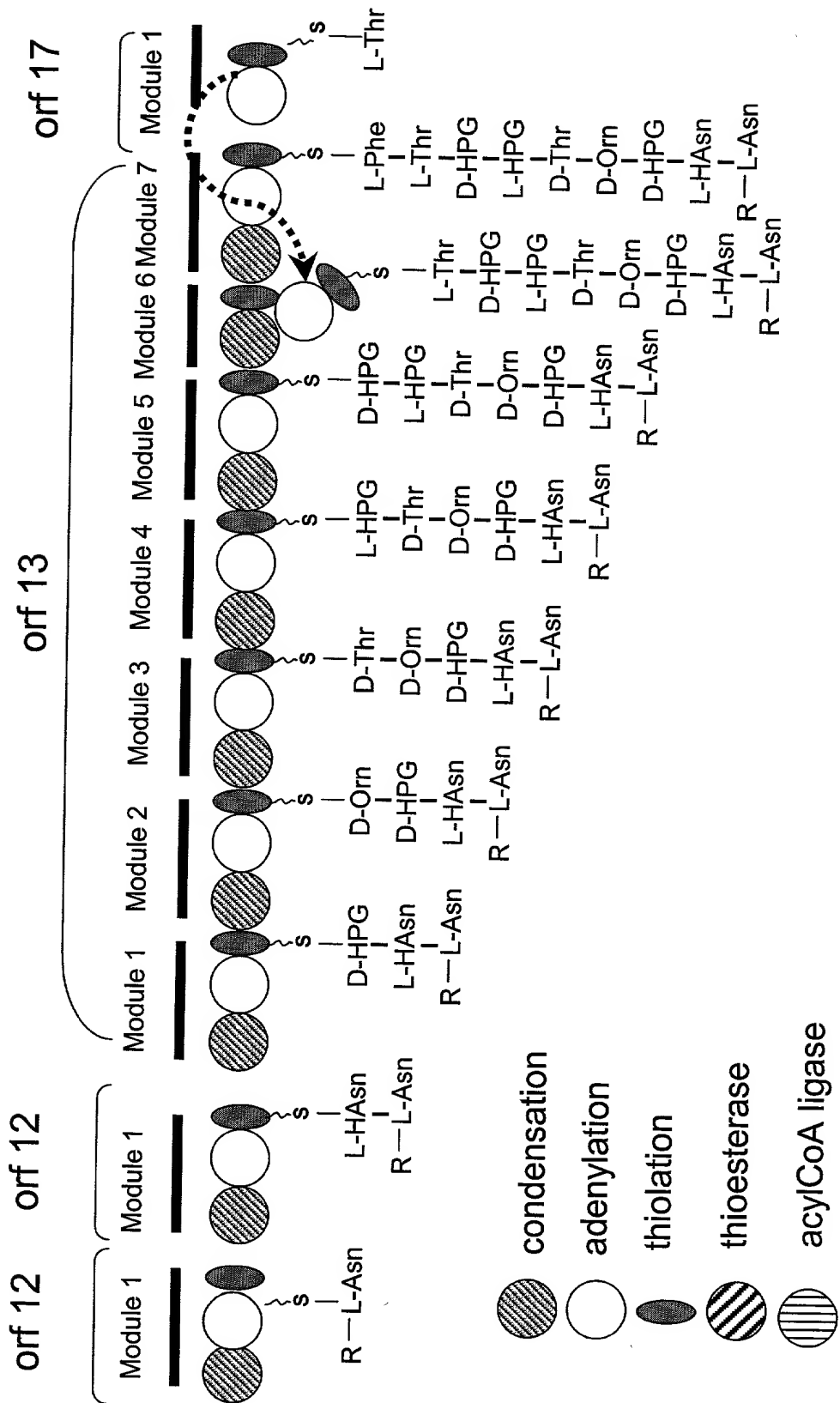


Figure 2A

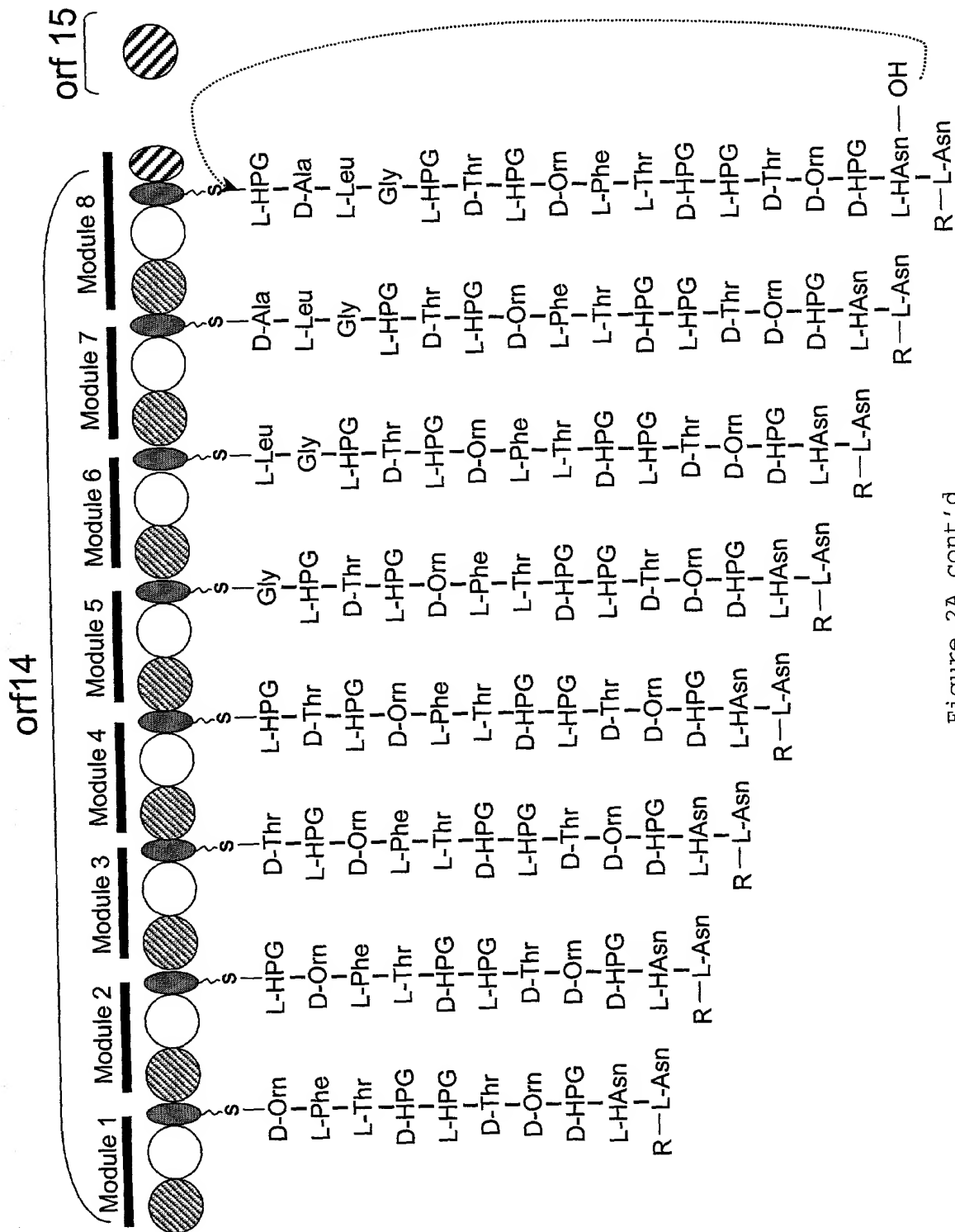
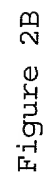
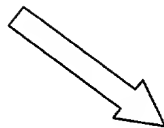


Figure 2A cont'd



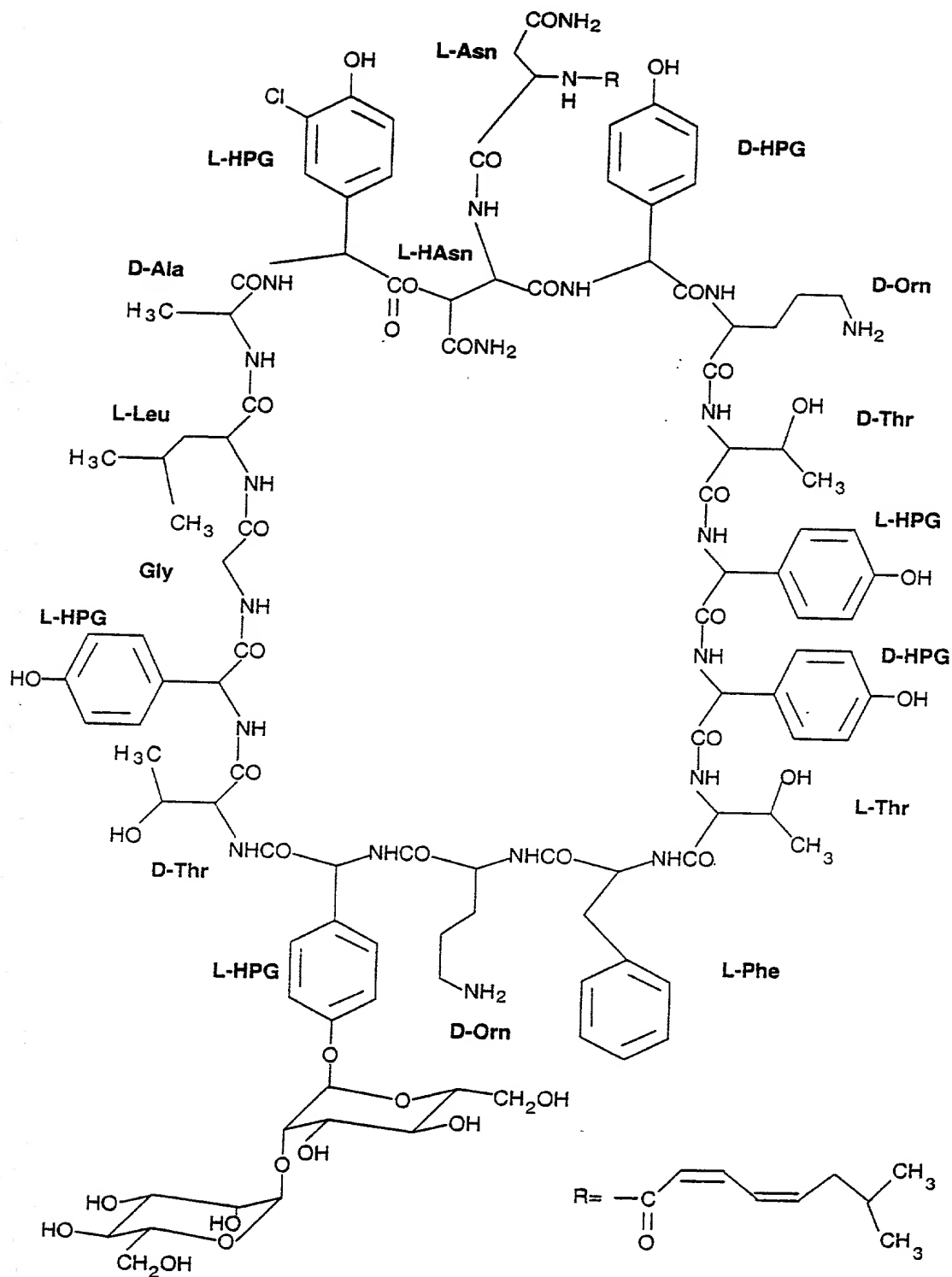


Figure 2C

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Orf12 -----ERRRLLDEWN-ATAAPSSDTVLARFEEQAARTPEAPAVVC
Orf13|M1 -----ERSRLLVEWNDTARPVVESSVPALFAKRVAATPDATAVVG
Orf13|M2 -----NATAVPAQPALVPELFTAQAARTPTWPAVLT
Orf13|M3 -----DRLLTAWNEAREPAPP-VTLPLDFDRQARRTPEAVALTA
Orf13|M4 -----EIERVVHSWNDTARPVVESSVPALFAEQVAAAPDATAVVG
Orf13|M5 -----ERSRLLVEWNDTARPVVESSVPALFAEQVAAAPDATAVVG
Orf13|M7 -----TVPELVAAQVARRPGAVALRS
Orf14|M1 -----NDTAAPAPAGLVPELFAAQAARTPDAAVAVAG
Orf14|M2 -----NDTARRVRQASVPELFAERVAAPGAPAVAA
Orf14|M3 -----EESRLMLAAGEEPAPALPEITVAALVAEQCARTPGAVAVTG
Orf14|M4 -----NETRRAVTRASVPELFAKQVAATPDAAVAVAG
Orf14|M5 -----ERRLVLTGWNDTTAAVPAVAVPELIERRAAAEPEAGAVWC
Orf14|M6 -----ERREVLRTPNATARDVAAATLPAIVGEWARTTPGATAVTA
Orf14|M7 -----EREAVLSGGNGGTAPVPVTTVPALFAEQARRTPGAVAALS
Orf14|M8 -----ERSRLLVEWNDTARPVVESSVPALFAERVAAPDATAVVG
Orf17 -----RTLTGLFAEQVAARPTAVAVSD
GrsA_Adomain MLNSSKSILIHAQNKGTHEEEQYLFVNNTKAEYPRDKTIHQLFEEQVSKRPNNVAIVC
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A1 A2
Orf12 GDVTVTYAELEAGANRLARVLRLARGAGPESVVALCLPRGPEVVTGILAAWKAGAAAYLPVD
Orf13|M1 EGVSWSYRELDORSDVLARRLVAGVGVESPVVVALERSPEVLSAFLAVAKAGGVFVPVD
Orf13|M2 AGAEMSIAELEERSNRLARWLAGRGVGADDRVALMMRRGPPELMVAAILAVLKAGAAAYLPVD
Orf13|M3 DGVSILTYRELSERANRLARLLTSRGIGPESLVGVVLPVSADLVVALLGVLAQAAYVVPVD
Orf13|M4 EGVSWSYRELDARSDALARSLVAGVGVESPVVVALERSPEVLSAFLAVAKAGGVFVPVD
Orf13|M5 EGVSWTYRELDARSDALARSLVAGVGVESPVVVALERSPEVLSAFLAVAKAGGVFVPVD
Orf13|M7 EDGEITYAELEARAGRLAAVLRRLRGIGPESRVAVLLPRGVEQVVAFLAVVRAGGTYLPID
Orf14|M1 PDRELTYAELEDERSGRLARWLIRRGVAADTRVALVLSAELPVAILAVLKAGGAYLPID
Orf14|M2 GDLFRTYADLDARSDALARSLVAGVTAESPVVVALERSADVLTAFLAVAKAGGVFVPVD
Orf14|M3 PDASLTIAELEDERAARIARWLRRHGAGPGAACVLMERSAELVAVLLGVMRAGAAYVVPVD
Orf14|M4 EGVSWSYRELDVRSDALARSLVAGVGIESPVVVALDRSPEVPTAFLAVAKAGGVFVPVD
Orf14|M5 GDTHLRYGELNARANRLARLLVERGAGPESIVAVCLERSADLVVTLAVLKAGGAYLPID
Orf14|M6 ENDRITYAELEARANRLARSLIARGVGPGAVVGMLLPRSPGLVAMLAIVKAGGAYLPID
Orf14|M7 EGMSLTIAADLAARVNRLARHLVSLGAGPETVVGIAISRGLDMLVAVLAVGQAGAAAYLPVD
Orf14|M8 EGVSWSYRELDORSDVLARSLVAGVGLESPPVVVALERSADVLTAFLAVAKAGGVFVPVD
Orf17 DRGHITYRELEWSGRLARGRLKAGVRDGDVAVGVCLDRSAELVAVLLAVLKAGAAAYPLD
GrsA_Adomain ENEQLTYHELVNKANQLARIFIEKGIGKDTLVGIMMEKSIDLFIGILAVLKAGGAYVPID
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Orf12 TELPAERVAYLLGDSAAAVRLG--TAETLAALPDGP-----AADVDVHA
Orf13|M1 LSWPQARVDAVVADCAARVAVA--DRPMSGLTVVVSAGL-----GGDSAVVSA
Orf13|M2 PDLPRDRVDYLLADAAPAFVLA--ERATAPWVPVA-----GGIPVLVVDA
Orf13|M3 ADYPAERIGYILGDAGAVCVLT--VDATEAGAVPPG-----VPKLVLDH
Orf13|M4 LSWPQARIDAVVADCAARVAVA--DRPMSGLTVVPA-----GGDSAVVSG
Orf13|M5 LSWPQARVDAVVADCGARIAVA--DRPMSGLTVVVSAGL-----GGDSAVVSG
Orf13|M7 PAYPRDRVDYLVDAEPACLLT--VAGHRAAAPAAP-----AVVELDD
Orf14|M1 PAQPPRRIADIVADAAPALVLA--QASTADVADASPALVLAPASDGVPTGAVPVHLLDS
Orf14|M2 LSWPRARVDAVIADCAAWIAVA--DRPMTGLTVVPAN-----VPCLAIID
Orf14|M3 PAYPAERIRFVVTDARAACVVS--ESASAGLVPDG-----VPCLAIID
Orf14|M4 LSWPQARVDAVIADCAARVAVA--DRPMTGLTVVPA-----AQRIVLGD
Orf14|M5 PGYPAGRIAYMLADARPALLVTSFAVASGDSLPDGG-----QRLLLDD
Orf14|M6 PGYPAPRLARMVEDAAPALLLA--TAGTADAVPAGP-----AAAVVLDE
Orf14|M7 PSYPDERKEFMLTDAGAAVYLT--LASDADRVPVPGTP-----VRLAPES
Orf14|M8 LSWPQTRIDAVIAD-S--RPVLVLDSVDLP-----VRLAPES
Orf17 AAYPADRIAYTVGDAGLAVVVV--TSADFPDV-DG-----VRLAPES
GrsA_Adomain IEYPKERIQYILDDSQARMLLT--QKHLVHLIHNIFQFN-----QQVEIFEE
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Figure 3A

A3

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Orf12      PEIARE-----SP-----SPLRLEPLPDQLAYVIYTSGSTGLSKGVGVSHGGLANYVGWAS
Orf13|M1   DLTADRAVVLPSRPVP-----GAAYRMYTSGSTGRPKGVVTHQNVLVDLAT---
Orf13|M2   PAVAAEVAHSGEAVTDRDRRAALRGHGLAYVIYTSGSTGRPKGVLIITHDGLANLTL-DH
Orf13|M3   PETVTALAACDTAPLGEAERAGELLPEHPAYVIYTSGSTGTPKGVLIPIHRNVVELFAATR
Orf13|M4   DQVGDSAVVLPAGPVP-----GAAYRMYTSGSTGRPKGVVTHQNVLVDLAT---
Orf13|M5   DLTADRAVVLPA GPVP-----GAAYRMYTSGSTGRPKGVVTHQNVLVDLAT---
Orf13|M7   PATAAEIADAEPEPP-----VAVRPTH SAYLIYTSGSTGRPKGVVTHRGVAALVATQA
Orf14|M1   PAVRDEVAQC PAGAVTDADRRGVLLGGHAAAYVIYTSGSTGRPKGVVSHDAFANLVL-DQ
Orf14|M2   -RAGDPAVALPPRPLP-----GAAAYRMYTSGSTGRPKGVVTHQNVLVDLT---
Orf14|M3   P-----AAAAEPAEPGD DPGDAAGPRDDPAYIYTSGSTGTPKGVVSHRNVVALLTATR
Orf14|M4   DAAGDPAAELPPRPLP-----GAEVYRMYTSGSTGRPKGVVTHQNVLVDLAT---
Orf14|M5   PDTAAALDGLAGTDLVLSERRGVTHPAHPAYVIYTSGSTGRPKGVVPHGALTNFVAAMS
Orf14|M6   PGTAAELARLDGDPIDREERTHPIRPGHPAYLMFTSGSTGRPKGVLPVPHAGIDRMVR-RS
Orf14|M7   PVTAAARIAGLDPADLTDADRVAPLLPAHRA YVIYTSGSTGRPKGVAVEHRTVVNLLSWAA
Orf14|M8   -----AAEADLPRVPA-----GAGVYRMYTSGSTGRPKGVVTHQNVLVDLAT---
Orf17      -----LAEAGDDPGIPLATPAG--PERPAYVIYTSGSTGRPKGVVPHANVSALLDATR
GrsA_Adomain DTIKIREGTLNHLVPSK-----STD LAYVIYTSGTTCNPKGTMLEHKGISNLKVFFE

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A4

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Orf12      VLYGGLSAP---LHSSLAEDLTVTSVFVPLVCGGSVVVSAAGGGRGLASLLAAGDG--FS
Orf13|M1   -DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNNGGTVVAPQRSID-ATVCLKDLIRAHDLT
Orf13|M2   GRFGLGPGARVAQFASPGFDMFVDEWSMALLAGAALTFVPPERL-GADLAAFLAEYGV
Orf13|M3   GSFHFGEDVWSWFHSAFDFSVWELWGALLHGGRVVMVPPFAVSRSPRDFWELLVREVT
Orf13|M4   -DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNNGGTVVAPQRSID-ATVLRDLIRGHELT
Orf13|M5   -DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNNGGTVVAPRRSID-ATVLRDLIGAHFLT
Orf13|M7   ERLAVTGESRVLQFASVGFDASTWEMVMALCAGATLVVAPADDLLPGPALAATLSGHAVT
Orf14|M1   RRLGIGPGSRVAQFASPGFDMFVDEWSMALLAGAALVIVPPERL-GADLAAFLTERGVT
Orf14|M2   -DRCWGPTPRVLFHAPHAFDASSFELWVPLLTGGTVVAPGESID-TGVLRLQIRAHFLT
Orf14|M3   PLFGFAGDEVWSWFHSAFDFSVWELWGALTHGGRVVVVPYAVSRSPRDFWELLVREGVT
Orf14|M4   -DTCWGPTPRVLFHAPHAFDASSYEIWVPLLNNGGTVVAPGRSID-AAVLGELIRAHFLT
Orf14|M5   DRLALGAGDRLLAVTTVAFDIHWLELYVPLVGGAGVVVAEDAVVRDPAAVAALLDRHAVT
Orf14|M6   TCIQLAPDDVPLPHLSSVSFDAATEIHWGALLNGATLAVAPAETLS-VAELRAFLADRAGT
Orf14|M7   GRFGGADFARTLAATSLNFDVSVEIFGPLVSGGSIEIVTDLLALADPASPAPWEA----S
Orf14|M8   -DTCWGSTPRVLFHAPHAFDASSYEIWVPLLNNGGTVVAPRRSID-ATVLRDLVRGHELT
Orf17      EEEYALGPGDVWTFHSAFDFSVWELWGCLLTGGHLVVVPYVWVSRSPQFHDLLAERGVT
GrsA_Adomain NSLNVTEDKDRIGQFASISFDSWVWEMFMALLTGASLYIILKDTINDFVKFEQYINQKET

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A5

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Orf12      LVRVVPGHRLRLAELVPAGEMA AVG---SLVAGGEVLAGGDVREWLSRVPGS--VVVNE
Orf13|M1   HVEVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVKDANPGL--RVROL
Orf13|M2   HATLPP---AVVGTIPDGVLPSPF-----VLIVGGDVLPGDLARR--WLRDGR--VLENS
Orf13|M3   VLSQTP---SAFYQLAAAA-DDTPD-ALRVVFGGEALDPGRLAGWRERRPDG-PRLVNM
Orf13|M4   HVEVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVKDANPGL--RVROL
Orf13|M5   HVEVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVKDANPGL--RVROL
Orf13|M7   HATLPP---AVLAASAPGD LAPLA-----VLVSAGEALGPD LVR--QFAPGR--ALVNA
Orf14|M1   HATLPP---AVVATLPEESLPRSF-----VLLIGGDALPDDLARR--WLRDGR--WLGNS
Orf14|M2   HVEVTA---GLLRVLA E-DPSCFAG--LTEVLTGGDVVPAEAVRRVLDANPGV--RVROL
Orf14|M3   VLSQTP---SAFAQLMAAAGDDDRD-ALRFVFGGEALDPGRLAGWLARRPK-PRLVNM
Orf14|M4   HVEVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVMEANPGL--RVROL
Orf14|M5   IVQATP---ALWQALLAGHADAVRD---VRLIVGGEALPPALAG--RMAAAGR--GVTNL
Orf14|M6   KLELT---GLLHEVIDADVTALAG--LKAVYTCGGDVLSPAHCRSLDRVPGL--ELVNA
Orf14|M7   LVSGVP---SAFSRVLDRGDIAART---RSVVLAGEALTADVNNATRAALPGV--RVANI
Orf14|M8   HVEVTA---GLLRVL---DPSCFAG--LTEVLTGGDAVSAEAVRRVKEANPGL--RVROL
Orf17      VLNQTP---SSFTQLVAADRGAEERDLAVRLVIFGGEPLDARTVLPWLD RRPPEARCRVNM
GrsA_Adomain VITLPP---TYVVHLDPERILSIQT-----LITAGSATSPSLVNKWEKVT-----YINA

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Figure 3A cont'd

	A5	A6	
Orf12	YGPTEVVVGC	SFVSAAGDVVGD--VVPVGRPVANTRLFVLDDEGLRPVPAGVAGELYVAG	
Orf13 M1	YGPTEVTLCA	TQHLLD-DG-----VPIGRPLDNTRVYVLDLQPVVPGVTGELYVAG	
Orf13 M2	YGPTEVTVNA	ATWR-AEAGDWGS--VAPIGTVPVNLRAYVLDGWLRPVPVPGADGELYVSG	
Orf13 M3	YGITETTVH	VTHQDLAPAD-TTG--S-PIGRGIPGLSVYVLDALRPVPPGVAGEVYVAG	
Orf13 M4	YGPTEVTLCA	TQHLLV-DG-----VPIGRPLDNTRVYVLDLQPVVPGVTGELYVAG	
Orf13 M5	YGPTEVTLCA	TQHLLD-DG-----VPIGRPLDNTRVYVLDLQPVVPGVTGELYVAG	
Orf13 M7	YGPTEVTVCA	TASAPLGPEDPPH----IGAPVADSRVYVLDLQPVVPGVTGELYVSG	
Orf14 M1	YGPTEVTVNA	ATWR-CEPGTWEG--ATPIGRPVANLRAYVLDGRLRPVPVPGVGEELYVSG	
Orf14 M2	YGPTEVTLCA	TQHVVREPSV----LPIGRPLDNTRVYVLDLQPVVPGVTGELYIAG	
Orf14 M3	YGITETTVH	TTYQHIAFG--TTG--S-VIGRGLPGFGLYVLDALRPVPAGVGEVYARG	
Orf14 M4	YGPTEVTLCA	TQVLDGTG-----VPIGRPLDNTRVYVLDLQPVVPGVTGELYVAG	
Orf14 M5	YGPTEVTVW	ATVADLGA-SPAG---PVPIGTPLRNTRAFVLDLQPVVPGVGEELYLAG	
Orf14 M6	YGPTEVTVI	TLHR-VREPDLDA	TGVPIGVPISTRVYVLDLQPVVPGVAGELYTSG
Orf14 M7	YGPTEATVY	STAWHTDR-DVTGG--AAPIGRPVNTNTRAYVLDLQPVVPGVGEELYLAG	
Orf14 M8	YGPTEVTLCA	TQHLLD-DG-----VPIGRPLDNTRVYVLDLQPVVPGVTGELYVAG	
Orf17	FGITETTVH	VTAVDVTRAAALAG--SRVGRPLPGWAVRVLDLQPVVPGVGEIYVGG	
GrsA_Adomain	YGPTEVTVI	CATTWVATKETIGHS--VPIGAPIQNTQIYIVDENLQKSVGEAGELCIGG	

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	A6	A7	A8	
Orf12	SQVARGYVGR	SGLTASRFVACPF	FG-VGERMYRTGDVVR	LAG-GDLVFFVGRVDEQVKIRGY
Orf13 M1	AGVARGYAG	MPGLTAERFVADPF	NT-GGRLYRTGDLVR	WTDGVLHFAGRADDQVKIRGY
Orf13 M2	AGLARGYIN	RAGLTAERFVACPF	EP-GERMYRTGDVVR	WTAEGRLVFAGRSDDQVKIRGF
Orf13 M3	RQLARAYIG	RAALTGTREVFAC	PLFAGERMYRTGD	RAWSR-GRLOFAGRTDDQVKIRGF
Orf13 M4	AGLARGYAG	MPGLTAERFVADPF	FSV-GGRLYRTGDLVR	WTDGVLHFAGRADDQVKIRGY
Orf13 M5	SGLARGYAG	MPGLTAERFVADPF	NT-GGRLYRTGDLVR	WADDGVLHFAGRADDQVKIRGY
Orf13 M7	ASLARGYAG	RAALTAERFVACPF	AP-GERMYRTGDRA	RWDAAAGRLTFAGRADDQVKIRGF
Orf14 M1	AGLARGYIN	RAGLTAGSFVACPF	EP-GERMYRTGDIVR	WDARGRLVYAGRADDQAKIRGF
Orf14 M2	AGVARGYAD	MPGTTAERFVADPF	FTA-GGRLYRTGDLVR	WTGEGELVFAGRADDQVKIRGY
Orf14 M3	PQVARGYIG	RPGLTAERFVASPF	AP-GERMYRTGDVAR	WTADGRLVFAGRSDDQIKIRGF
Orf14 M4	AGLARGYAG	MPGLTAERFVADPF	SS-GGRLYRTGDLVR	WTDGVLVFAGRADDQVKIRGY
Orf14 M5	DQLARGYH	GRAGLTAERFVADPF	FG-RGERMYRTGDR	VRWTRGGSLEFLGRVDDQVKIRGF
Orf14 M6	IGLAHGYAG	RPAFTAERFVACPF	AP-GERMYRTGDLVR	WTADGRLVFAGRADNQVKIRGF
Orf14 M7	AQLARGYL	GRPLTGGERFVACPF	FGPGGERMYRTGDR	VRWNADGDLVFAGRADDQVKIRGF
Orf14 M8	SGLARGYAG	MPGLTAERFVADPF	FSV-GGRLYRTGDLVR	WTDGVLHFAGRADDQVKIRGY
Orf17	AGVAIGYIN	RPELTAERFVTG---	PDGRRWYRSGDRGR	LLPDGTLLEHLGRLLDQVKIRGF
GrsA_Adomain	EGLARGYWK	RPELTSQKFVDNPF	VPE-GEKLYKTGDQAR	WLSDGNIEYLGRIDNQVKIRGH

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	A8	A9	
Orf12	RVEPDEVRLV	VAGHPRVAGAAVVARPD	AVGE---RQLVAYVVAAGEPAG---LAESVRAH
Orf13 M1	RVEPGEVEAV	LAQHDPVVSQVAVVRED	TPGD---KRLVAYVVGG-----DIEAY
Orf13 M2	RIEPGEVEAV	LAAGPGVSQA	AVVREDVPGD---KRLVAYVVGG---D---VEALRSY
Orf13 M3	RIEPGEVQAV	VAAHPEIAAAAVVRED	VPGD---PRLTAYVVPAGPRTAPAAVAETVRRF
Orf13 M4	RVEPGEVEAV	LAQHDPVVSQVAVVRED	TPGD---KRLVAYVVGG-----DVEAY
Orf13 M5	RVEPGEVEAV	LAQHDPVVSQVAVVRED	TPGD---KRLVAYVVGG-----DVEAY
Orf13 M7	RVEPGEVA	AVLGEHPAVARA	AVVARTDGPQG---ARLVAYLVAAADP---AGPDAAAVRAY
Orf14 M1	RVEPGEVEAV	LAAGPGVNQVAVVRED	VPGD---KRLVAYVVGG---D---VETLRSY
Orf14 M2	RVEPGEVEAV	LAALPGVSQA	AVVREDVPGD---KRLVAYLVAAPE-----TVEAARAH
Orf14 M3	RIEPGEVEAV	LAAGPGVSQA	AVVREDVPGD---KRLVAYVVGG-----DAETLRSH
Orf14 M4	RVEPGEVEAV	LAAPDVAQVAVVRED	TPGD---KRLVAYVVGG-----DVEAY
Orf14 M5	RIELGEVEA	LAALAFGVPVAAAAVRED	VPGD---RRLVGYVVPVAAAGEPE---PDPAAVRAH
Orf14 M6	RVEPGELETV	LSGHPAVARA	AVLAREDTPGA---KRLVAYVVPARPDEDGDALAESVRAH
Orf14 M7	RIEPGEVQAV	VARQAGVARAVVLARS	SDSPGD---ARLVAYVVPADRDADRRALAATVRS
Orf14 M8	RVEPGEVEAV	LAQHDPVVSQVAVVRED	APGD---KRLVAYVVGG-----DVEAY
Orf17	RIELDEIRG	SVLTECAGVAAAVVIR	STPDDPATARLDAYVVAEAG-----ATPPVAEH
GrsA_Adomain	RVELEEVE	SILLKHYISETAVSV	HKDHQEQ---PYLCAYFVSEKHIP-----LEQLRQF

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Figure 3A cont'd (2)

A10

Orf12	VAERLPEYMPVAAVVTLDLDEIPLTVNGKVDRAALPEP-----
Orf13 M1	GQERLPGYMPVSAFVHLDALPLTSSNQKVDRAALPAPSMESG-----
Orf13 M2	AQQRLPGYMPVSAFVELDRLPLTVNGKLDRAALPVVDLARG-----
Orf13 M3	AADRLPAYMLPSAVVVLDALPLTDHGKLDRAALPAPQHT-----
Orf13 M4	AQERLPGYLVPSAFVHLDALPLTSSNQKVDRAALPAPSVESGV-----
Orf13 M5	AQERLPGYMPVSAFVQLDALPLTSSNQKVDRAALPAPSMESG-----
Orf13 M7	AAATLPAHLLPAAFVPLDRLPLTVNGKLDRAALPEPETGAG-----
Orf14 M1	AQQRLPGYLVPSAIVALAELPLTSSAKVDRAALPVVD-----
Orf14 M2	AEQRLPSYLVPSAFVQLDALPLTGNQKVDRAALPAP-----
Orf14 M3	AQQRLPGYLVPSAFVELDRLPLTVNGKLDRAALPVVD-----
Orf14 M4	AQERLPGYLVPSAFVHLDALPLTSSNQKVDRAALPAPSVESG-----
Orf14 M5	VAAQLPAYMPVSAVVVLPDLPLTANGKLDRAALPAPDYGAASAGRAPADE--
Orf14 M6	AARQVPDYLMPAATVVLPDLPLTSSGKVDRAALPAPDVPGG-----
Orf14 M7	TARELPAYLVPAVVVLDLPLTVNGKLDRAALPAPGL-----
Orf14 M8	AQERLPGYMPVSAFVHLEALPLTANGKVDRAALPAPE-----
Orf17	AARMLPAYMCPATFTFLDALPMTENGKVDRAALPEP-----
GrsA_Adomain	SSEELPTYMIPSYFIQLDKMPLTSSNGKIDRKQLPEPDLTFGMRVDYEAPRNE

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Figure 3A cont' d (3)

		235	236	239	278	299	301	322	330	
	Orf13 M1 HPG	D	A	Y	H	L	G	L	L	HPG
	Orf13 M4 HPG	D	A	Y	H	L	G	L	L	
	Orf13 M5 HPG	D	A	Y	H	L	G	L	L	
	Orf14 M2 HPG	D	A	F	H	L	G	L	L	
	Orf14 M4 HPG	D	A	Y	H	L	G	L	L	
	Orf14 M8 HPG	D	A	Y	H	L	G	L	L	
emb	CAB38518.1 Cda1 M6 HPG	D	V	Y	H	L	G	L	L	
emb	CAA11795.1 CepB M2 HPG	D	A	V	H	L	G	L	L	Thr
emb	CAA11795.1 CepB M1 HPG	D	I	F	H	L	G	L	L	
	Orf13 M3 Thr	D	F	W	S	V	G	M	V	
	Orf14 M3 Thr	D	F	W	S	V	G	M	V	
	Orf17 M1 Thr	D	F	W	N	I	G	M	V	
gb	AAC38442.1 AcmB M1 Thr	D	F	W	N	V	G	M	V	
emb	CAB38518.1 Cda1 M2 Thr	D	F	W	N	V	G	M	V	
emb	CAA09819.1 FenD M2 Thr	D	F	W	N	I	G	M	V	
	Orf13 M2 Orn	D	M	D	T	D	G	S	V	Orn
	Orf14 M1 Orn	D	M	D	T	D	G	S	V	
gb	AAC06347.1 BacB M1 Lys	D	A	E	S	I	G	S	V	
gb	AAC82550.1 FxbC M1 5hOrn	D	M	E	N	L	G	L	I	
gb	AAC82550.1 FxbC M3 5hOrn	D	M	E	N	L	G	L	I	Asn
	Orf12 M1 Asn	D	L	T	K	V	G	E	V	
emb	CAB38517.1 Cda2 M3 Asn	D	L	T	K	V	G	E	V	
gb	AAC06348.1 BacC M5 Asn	D	L	T	K	I	G	E	V	
gb	AAC45930.1 TycC M1 Asn	D	L	T	K	I	G	E	V	Phe
	Orf13 M7 Phe	D	A	W	T	V	A	A	V	
emb	CAA33603.1 GrsA M1 Phe	D	A	W	T	I	A	A	I	
gb	AAC45929.1 TycB M3 Phe	D	A	W	T	I	A	G	V	
gb	AAC06348.1 BacC M2 Phe	D	A	F	T	V	A	A	V	Gly
	Orf14 M5 Gly	D	I	L	Q	L	G	L	V	
emb	CAB38517.1 Cda2 M2 Gly	D	I	L	Q	L	G	L	I	
emb	CAB15186.1 DhbF M1 Gly	D	I	L	Q	L	G	L	I	
gb	AAF17280.1 NosC M2 Gly	D	I	L	Q	L	G	L	I	Leu
	Orf14 M6 Leu	D	A	F	F	Y	G	A	T	
emb	CAA82227.1 CssA M2 Leu	D	A	W	L	Y	G	A	V	
emb	CAA82227.1 CssA M3 Leu	D	A	W	L	Y	G	A	V	
gb	AAC06346.1 BacA M3 Leu	D	A	W	F	L	G	N	V	(Ala)
	Orf14 M7 (Ala)	D	V	F	S	V	A	I	V	
gb	AAC06348.1 BacC M2 Phe	D	A	F	T	V	A	A	V	
gb	AAC83656.1 PchE M1 Cys	D	L	F	N	L	S	L	I	
emb	CAA82227.1 CssA M11 Ala	D	V	F	I	Y	A	A	I	

Figure 3B

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

-----MVIDAATQPTVPDAFRAQ
-----MAMSVRSLPAALRAC
MKTNSSFHAAGEVATQPAWGTGEQAAQPLNGSTSRFAMSESSLADLLQKA
-----MSRPAGIVDIARRH
-----MACRPDSLHASAVTSRRRMRHTLVELLQER
-----MYTSQFQTLVDVIRNR
:
:

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

AIARPGEPALVVLPG--DPDAEPVTLTYAELDRRAAARAAWLAARFPAGE
ACLQPHDPAFTFMDYEQDWDGVAITLTWSQLYRRTLNVARELSRCGSTGD
ASQYPNRAAYKFIDYDTPAGFTETVTWQVHRRAMIVAEELWIYASSGD
AERTPARPAYAFLP---DGETESVRFVSFADIDRRARAVAVALQDRGLAGE
ALSEPRHEAFTFLG---EAGVPAVRVDYSSMDVLARAIAARLQADGRVGE
SNIS--DRGIRFIE---SDKIETFSYRQLFDEAQGFLGYLQHIGIQPK
:
: . : . : . : *

AL1

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

R-ILIALPTGAEFVELYLACLYAGLVAVPAPPPGGS--SGASERTVGIAA
R-VVISAPQGLEYYVVAFLGALQAGRIAVPLSVPQGG---VTDERSDSVLS
R-VAILAPQGLEYYIAFMGVLAQGLIAVPLPVPQFG---IHDERISSALR
R-VLVAYSPGPEYVQAFGLGCLYAGVVAVPQDEPR-S--GPSAERLAGIRA
R-ALLLYAPGPEYVAAFFGCLYAGVVAVPVYPPDTARLERSLLRLRTVAR
QEIVFQIQENKSEFVVAFWACLLGGMIFVPVVSIGEDNDHKLKVIRIWNILN
:
: . : . : . * . * . : . *

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

DCSPALAVVN---ADDAAPLTA-----VLRERGLSGLPVGALPPLAAE
DSSPVAILTTS---SAVDDVVQ---HVARRPGESPPIIEVDLLDLDPAN
DSAPSIILTTS---SVIDEVTYAPHACAAQGSAPIVVAVDALDLSSSR
DARPALALTA---GAPEAGLA-----GLATLDVAGVPDASAAG
DSRASVVLTTSFLOGLAGAMFEL-----APELGELSWVATDGTIALEAG
NPFLLASETVLDKMKKFAADHD-----LQDFHHQLIEKSDIIQDRIYD
:
:

AL2

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

AIRPPRGPRPDSLAVLQYSSGSTGSPKGVMLSHRAVLANLRAFDRSSGHN
GYTFKEDE-YPSTAYLQYTSGSTRTTPAGVVMHQNVVNFQELMSGYFAD
ALDPTRFE-RPSTAYLQYTSGSTRAPAGVVLSHKNVITNCVQLMSDYIGD
AWTDPVAG-PDALAFLOQYTSGSTRRPRGVMVGHGNLLANERCIAAACGHD
AWKPPGLS-GDSVAFLOQYTSGSTADPKGVVLTHRNLMHNLVSIHERFQLN
HPASQYEPEADELAFIQFSSGSTGDPKGVMLTHHNLHNTCAIRNALAID
* : : : * * * : * : * :
:

AL3

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

SDDVF-----GSWLPLHDMGLFAMLTAGLLNGAGVVLMSPTAFVRRPA
TDGIPPPNSALVSWLPPFYHDMGLVIGICAPILGGYPAVLTSPVSFLQRP
SEKVP---STFVSWLPPFYHDMGLMGIILPMINQDTAVLMSPMFLQRP
RDSTF-----VGWAPFFHDMGLVANLLQPLYLGLSVLMPMAFLQRP
RGSRG-----VIWLPPFYHDMGLIGVLTPIFGGLPVDLMSPLSFLQEPL
LKDTL-----LSWMPLTHDMGLIACHLVPALAGINQNLMPTELFIIRPI
* * * * * * * * * * * * * * * *
* . . : : . *

Figure 3C

AFGVPAP--DERIVLQEVHPRTPLDLPR----VASAVSRRLTVSFGV
AISVPGDRRTEKLVAIIELKKRGSDQDEAMARLGAIKREVTALSSSHGL
AIAVPDDR-TEKLVTLIELMKRGRTDDEEKNRLRTVKREVASAISRSHL
AFAPVPGDG-AERLVLVCELTSTRAYDPAA-----VBAVRAALAAHRGV
VFSVSVGA-SEEVVVVQEVDRYPGGDWDPD-----VIAAIRRDISQHAL
ACGVYDQETRSREIVLFAVIYKKSADRFAP-----LVKDIKKHLYQRGGW

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AL8

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

PVRNLLVRRGTVRRITSGKIRRTAVRERFLAGGITALHAELEPALRPVQ
SVADLVIVAPGSIPTTSGKVRRGACVEQYRQDQFARLDA-----
RVADVVMVAPGSIPTTSGKVRRSASVERYLHHEFSRLDAMA-----
APHTLVVLRGGIPKTTSGKVRRGHCRITAYLDGTLVPVHTAVRLP-----
RVHAVVLIKSGSLLKTSSGKVQRGATREAYLEGQLDTSADAAQEPVGE-
SIKEILPIR--KLPKTTSGKVRRYELAEQYESGKFALESTKIKEFLEG--
:: : : *::*:~* : : :

Orf26
gb|AAB52538.1|acyl_CoA_L|Mb
emb|CAB05426.1|fadD29|Mt
gb|AAG02359.1|blmVI|M1|Sv
gb|AAC44128.1|safB|M1|Mx
gb|AAF08795.1|MycA|M1|Bs

AGAGR

Figure 3C cont'd (2)

2040E0"6509/660

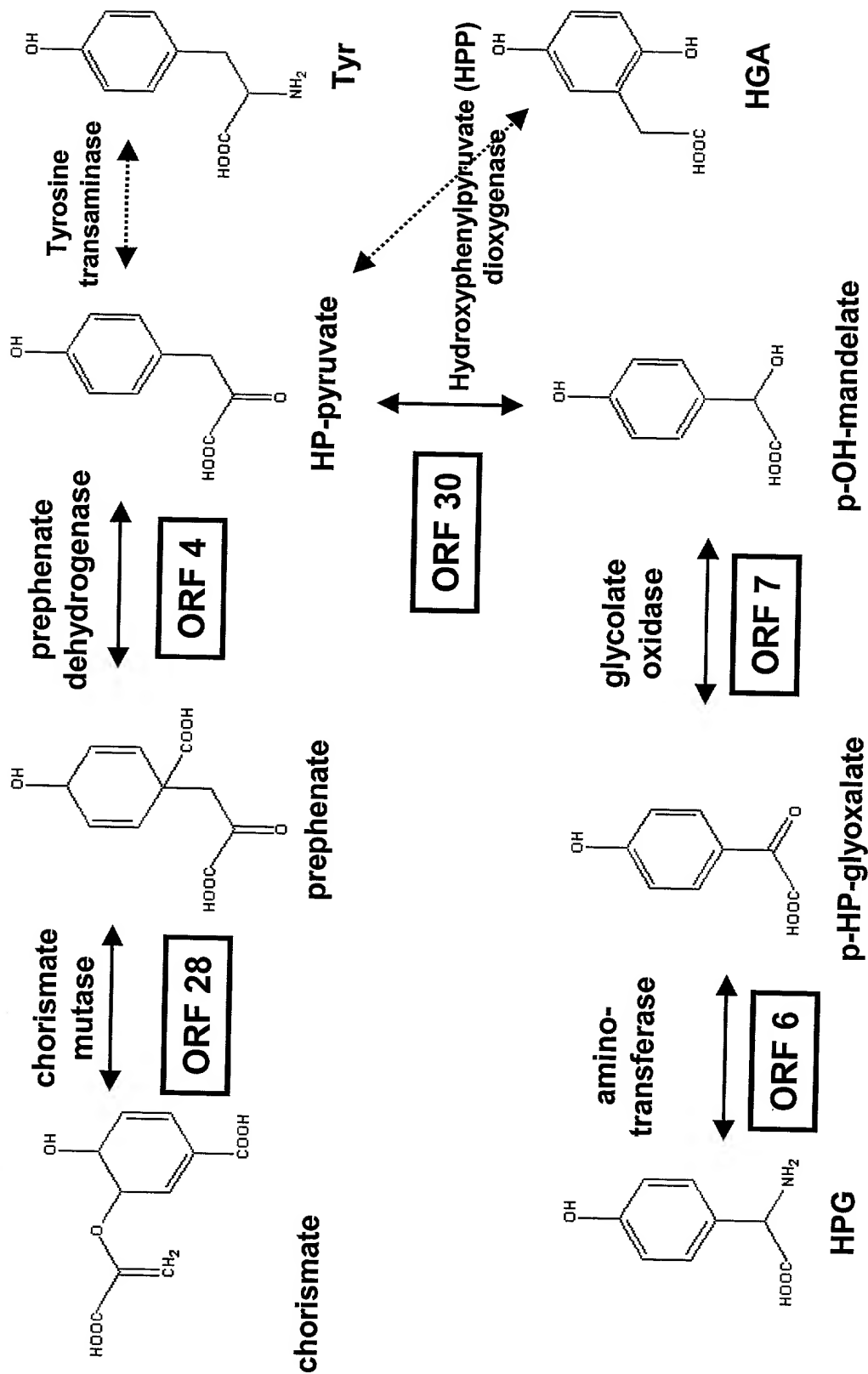


Figure 4

pfam00753
 1SML
 ORF 10

LVEDDDGAALIDTGFTAPAAKALLRLLKDG-- GKKIDAILLTHAHADHIGGVPELLER
 LVQTPDGAVLLDGGMPQMASHLLDNMKARGVTPRDLRLILLSAHADHAGPVAELKRR
 VMQTEQAAVVTDG-FISTDNRHGDRYTLDDL- PDHIDLVLITHGHQDHIVLETLLQLR
 ::: :*. : * : : : : : : : : : : : : : : : *

Figure 5A

pfam00067
 ORF 10

DPE--RFLDEN- GKFKKSYAFLPFGAGPRNCLGERLARMELFLFLATLLQRFEL
 DPVLYRYIRDHVGQVD----- MAFL-G-MEODGAPLNWLYKGLLTKPVNKKMSAS
 ** *:: : *:: *

Figure 5B

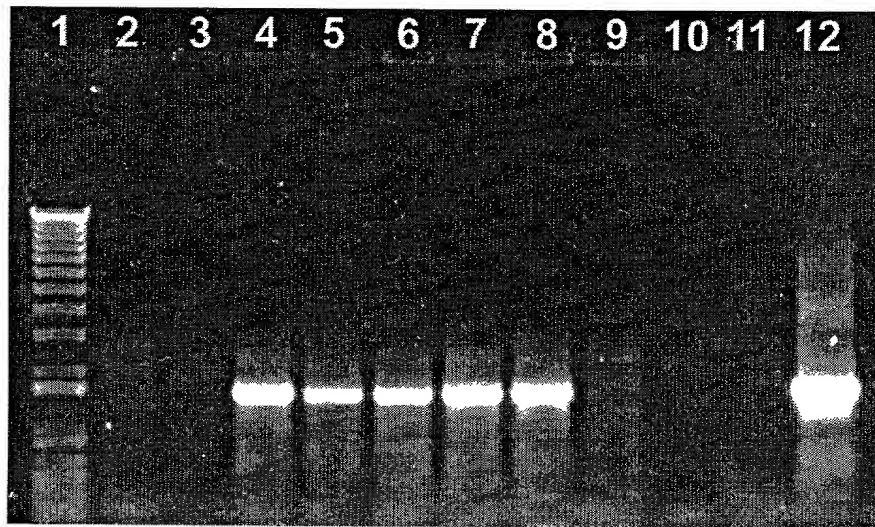


Figure 6

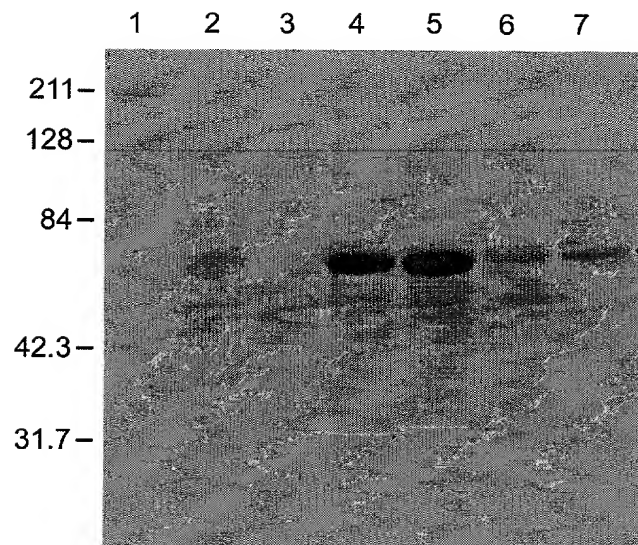


Figure 7

2040ED 6509/660